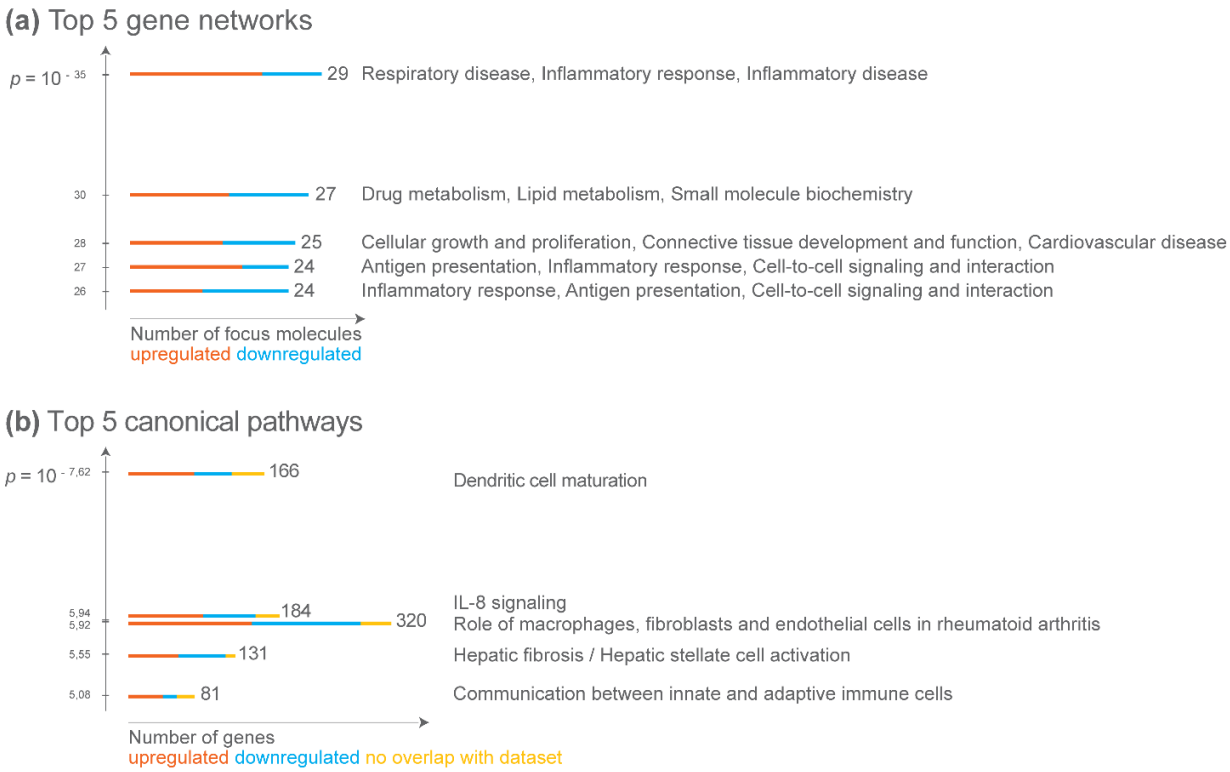
Supplementary Figure S1



Supplementary FIGURE S1: The top 5 gene networks and canonical pathways in FECD, based on MEA data. **(a)** The top 5 *gene networks*, based on IPA analysis of MEA data indicated a role for 'inflammatory response', 'inflammatory disease' and 'antigen presentation'. FDR-corrected *p*-values are displayed on a logarithmic y-axis (most significant results at the top). The 4th ranked gene network was centered on HLA-DR and other MHC class II molecules (Fig. 2). (Each gene network is composed of 3 '*functions*' that have ≥ 1 focus molecule in common. The number of focus molecules indicates the number of eligible molecules from the MEA data that are part of the gene network.) **(b)** The top 5 *canonical pathways* in FECD, indicated a role for 'dendritic cell maturation' (Fig. 1[d]), 'macrophages' and 'hepatic stellate cell activation'. The relative proportion of upregulated (orange) and downregulated (blue) genes was comparable across the different canonical pathways.

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